

## SCORE Search Results for Application 09529043

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### Item Listing Version# 1

Item Name	Download Content
<a href="#">us-09-529-043b-2.rag</a>	<a href="#">Download</a>
<a href="#">us-09-529-043b-2.rai</a>	<a href="#">Download</a>
<a href="#">us-09-529-043b-2.rapbm</a>	<a href="#">Download</a>
<a href="#">us-09-529-043b-2.rapbn</a>	<a href="#">Download</a>
<a href="#">us-09-529-043b-2.rpr</a>	<a href="#">Download</a>
<a href="#">us-09-529-043b-2.rup</a>	<a href="#">Download</a>

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OM protein - protein search, using sw model

Run on: February 28, 2006, 10:43:41 ; Search time 190 Seconds  
(without alignments)  
2636.273 Million cell updates/sec

Title: US-09-529-043B-2  
Perfect score: 5787  
Sequence: 1 VSTHTSSTLPAFKKILVANR.....RVVVPAAATKVEGGDLIVVVS 1140

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	5787	100.0	1141	3	AAB01436	Aab01436 Pyruvate
2	5784	99.9	1140	4	AAB67129	Aab67129 Corynebac
3	5784	99.9	1140	4	AAG90511	Aag90511 C glutami
4	5784	99.9	1140	5	AAE25601	Aae25601 Corynebac
5	5784	99.9	1140	5	AAU98053	Aau98053 Corynebac
6	5784	99.9	1140	7	ABU10426	Abu10426 Corynebac
7	5784	99.9	1140	9	AEB13171	Aeb13171 C. glutam
8	5778	99.8	1140	2	AAW93971	Aaw93971 C. glutam

9	5776	99.8	1140	4	AAG93249	Aag93249	C glutami
10	5762	99.6	1140	5	AAU98052	Aau98052	Corynebac
11	5762	99.6	1157	5	AAU98050	Aau98050	Corynebac
12	5756	99.5	1140	9	ADY49875	Ady49875	C. glutam
13	5756	99.5	1140	9	ADY80483	Ady80483	Ver3 poly
14	5756	99.5	1140	9	AEA26147	Aea26147	Polyester
15	5304.5	91.7	1139	4	AAB83180	Aab83180	Corynebac
16	4647.5	80.3	1141	6	ABU25961	Abu25961	Protein e
17	3791.5	65.5	1127	6	ABU34026	Abu34026	Protein e
18	3712.5	64.2	1127	6	ABU36886	Abu36886	Protein e
19	3712.5	64.2	1127	6	ABU34760	Abu34760	Protein e
20	3483	60.2	1124	7	ADB74261	Adb74261	Mycobacte
21	2624	45.3	532	4	AAB79302	Aab79302	Corynebac
22	2552	44.1	1144	6	ABU24853	Abu24853	Protein e
23	2541.5	43.9	1178	9	AEA62607	Aea62607	Mitochond
24	2526	43.6	1148	6	ABU18942	Abu18942	Protein e
25	2525.5	43.6	1150	8	ADS28305	Ads28305	Bacterial
26	2524.5	43.6	1178	7	ADE62415	Ade62415	Rat Prote
27	2524.5	43.6	1178	7	ADE62419	Ade62419	Rat Prote
28	2524	43.6	1148	4	AAU00511	Aau00511	Bacillus
29	2524	43.6	1148	8	ADS44682	Ads44682	Bacterial
30	2520.5	43.6	1178	7	ADE62421	Ade62421	Human Pro
31	2520.5	43.6	1178	7	ADE62417	Ade62417	Human Pro
32	2520.5	43.6	1178	7	ADJ68421	Adj68421	Human hea
33	2517.5	43.5	1178	9	AEA81227	Aea81227	Human pyr
34	2517.5	43.5	1178	9	AEA81226	Aea81226	Human pyr
35	2493	43.1	1146	5	ABB47612	Abb47612	Listeria
36	2493	43.1	1146	6	ABU32564	Abu32564	Protein e
37	2491.5	43.1	1144	6	ABU24164	Abu24164	Protein e
38	2491.5	43.1	1144	8	ADN25113	Adn25113	Bacterial
39	2488	43.0	1147	4	AAU33972	Aau33972	Staphyloc
40	2488	43.0	1150	6	ABU16467	Abu16467	Protein e
41	2485	42.9	1156	6	ABM73249	Abm73249	Staphyloc
42	2472.5	42.7	1142	4	AAU35213	Aau35213	Enterococ
43	2471.5	42.7	1147	8	ADS22417	Ads22417	Bacterial
44	2471.5	42.7	1151	8	ADS25784	Ads25784	Bacterial
45	2471.5	42.7	1151	8	ADS25973	Ads25973	Bacterial

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OM protein - protein search, using sw model

Run on: February 28, 2006, 10:51:37 ; Search time 50 Seconds  
 (without alignments)  
 1885.005 Million cell updates/sec

Title: US-09-529-043B-2  
 Perfect score: 5787  
 Sequence: 1 VSTHTSSTLPAFKKILVANR.....RVVVPAAATKVEGGDLIVVVS 1140

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
 1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*  
 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.			%		Query		Description
	Score	Match	Length	DB	ID		
1	5784	99.9	1140	2	US-09-220-081-2	Sequence 2, Appli	
2	5784	99.9	1140	2	US-09-677-575-2	Sequence 2, Appli	
3	5784	99.9	1140	2	US-10-045-072-2	Sequence 2, Appli	
4	3483	60.2	1124	2	US-08-311-731A-10	Sequence 10, Appl	
5	2520.5	43.6	1210	2	US-09-949-016-7176	Sequence 7176, Ap	
6	2520.5	43.6	1210	2	US-09-949-016-7177	Sequence 7177, Ap	
7	2464	42.6	1151	2	US-09-710-279-2448	Sequence 2448, Ap	
8	2464	42.6	1154	2	US-09-134-001C-3428	Sequence 3428, Ap	
9	2463.5	42.6	1163	2	US-09-134-000C-5707	Sequence 5707, Ap	
10	2174	37.6	973	2	US-09-107-532A-4810	Sequence 4810, Ap	
11	2038.5	35.2	895	2	US-09-270-767-42010	Sequence 42010, A	

12	1212.5	21.0	586	2	US-09-902-540-14597	Sequence 14597, A
13	1192	20.6	694	2	US-09-433-043B-126	Sequence 126, App
14	1165	20.1	475	2	US-09-248-796A-17094	Sequence 17094, A
15	1083	18.7	456	2	US-09-634-238-276	Sequence 276, App
16	1043.5	18.0	593	2	US-09-433-043B-122	Sequence 122, App
17	1036.5	17.9	447	1	US-08-611-107-6	Sequence 6, Appli
18	1036.5	17.9	447	1	US-08-422-560A-6	Sequence 6, Appli
19	1036.5	17.9	447	2	US-08-468-793-6	Sequence 6, Appli
20	1004.5	17.4	453	1	US-08-611-107-8	Sequence 8, Appli
21	1004.5	17.4	453	1	US-08-422-560A-8	Sequence 8, Appli
22	1004.5	17.4	453	2	US-08-468-793-8	Sequence 8, Appli
23	1002.5	17.3	453	2	US-09-433-043B-121	Sequence 121, App
24	995.5	17.2	453	1	US-07-956-700B-6	Sequence 6, Appli
25	995.5	17.2	453	1	US-08-476-537-6	Sequence 6, Appli
26	995.5	17.2	453	1	US-08-485-607-6	Sequence 6, Appli
27	995.5	17.2	453	1	US-08-475-879-6	Sequence 6, Appli
28	995.5	17.2	453	2	US-09-433-043B-6	Sequence 6, Appli
29	971	16.8	664	2	US-09-902-540-12181	Sequence 12181, A
30	968	16.7	474	2	US-09-328-352-7562	Sequence 7562, Ap
31	966.5	16.7	1116	2	US-09-252-991A-24374	Sequence 24374, A
32	961	16.6	453	2	US-09-543-681A-5871	Sequence 5871, Ap
33	952	16.5	605	2	US-09-433-043B-123	Sequence 123, App
34	944.5	16.3	451	2	US-09-540-236-3047	Sequence 3047, Ap
35	942.5	16.3	455	2	US-09-583-110-3905	Sequence 3905, Ap
36	939.5	16.2	477	2	US-09-107-433-3353	Sequence 3353, Ap
37	938	16.2	448	1	US-08-074-121-3	Sequence 3, Appli
38	938	16.2	448	4	PCT-US94-06447-3	Sequence 3, Appli
39	937	16.2	427	1	US-07-956-700B-3	Sequence 3, Appli
40	937	16.2	427	1	US-08-476-537-3	Sequence 3, Appli
41	937	16.2	427	1	US-08-485-607-3	Sequence 3, Appli
42	937	16.2	427	1	US-08-475-879-3	Sequence 3, Appli
43	937	16.2	427	2	US-09-433-043B-3	Sequence 3, Appli
44	935.5	16.2	454	2	US-09-198-452A-197	Sequence 197, App
45	935.5	16.2	457	2	US-09-438-185A-184	Sequence 184, App

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OM protein - protein search, using sw model

Run on: February 28, 2006, 10:52:31 ; Search time 177 Seconds  
(without alignments)  
2691.104 Million cell updates/sec

Title: US-09-529-043B-2  
Perfect score: 5787  
Sequence: 1 VSTHTSSTLPAFKKILVANR.....RVVVPAATKVEGGDLIVVVS 1140

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		ID	Description
	No.	Score	Match	Length	DB			
1	5784	99.9	1140	3	US-09-974-973-19		Sequence 19, Appl	
2	5784	99.9	1140	3	US-09-738-626-4265		Sequence 4265, Ap	
3	5784	99.9	1140	4	US-10-045-072-2		Sequence 2, Appli	
4	5784	99.9	1140	6	US-11-136-887-19		Sequence 19, Appl	
5	5762	99.6	1157	3	US-09-974-973-2		Sequence 2, Appli	
6	5762	99.6	1157	3	US-09-974-973-4		Sequence 4, Appli	
7	5762	99.6	1157	6	US-11-136-887-2		Sequence 2, Appli	
8	5304.5	91.7	1139	6	US-11-073-550-24		Sequence 24, Appl	
9	4647.5	80.3	1141	4	US-10-282-122A-53885		Sequence 53885, A	
10	3791.5	65.5	1127	4	US-10-282-122A-61950		Sequence 61950, A	
11	3712.5	64.2	1127	4	US-10-282-122A-62684		Sequence 62684, A	

12	3712.5	64.2	1127	4	US-10-282-122A-64810	Sequence 64810, A
13	2624	45.3	532	4	US-10-781-014-120	Sequence 120, App
14	2552	44.1	1144	4	US-10-282-122A-52777	Sequence 52777, A
15	2541.5	43.9	1178	5	US-10-972-963-45	Sequence 45, Appl
16	2526	43.6	1148	4	US-10-282-122A-46866	Sequence 46866, A
17	2525.5	43.6	1150	4	US-10-369-493-17338	Sequence 17338, A
18	2524	43.6	1148	4	US-10-369-493-23112	Sequence 23112, A
19	2520.5	43.6	1178	4	US-10-408-765A-227	Sequence 227, App
20	2517.5	43.5	1178	6	US-11-019-829-93	Sequence 93, Appl
21	2517.5	43.5	1178	6	US-11-019-829-94	Sequence 94, Appl
22	2517.5	43.5	1178	6	US-11-009-554-24	Sequence 24, Appl
23	2517.5	43.5	1178	6	US-11-009-554-25	Sequence 25, Appl
24	2493	43.1	1146	4	US-10-282-122A-60488	Sequence 60488, A
25	2491.5	43.1	1144	4	US-10-369-493-7766	Sequence 7766, Ap
26	2491.5	43.1	1144	4	US-10-282-122A-52088	Sequence 52088, A
27	2488	43.0	1147	3	US-09-815-242-5468	Sequence 5468, Ap
28	2488	43.0	1150	4	US-10-282-122A-44391	Sequence 44391, A
29	2472.5	42.7	1142	3	US-09-815-242-10806	Sequence 10806, A
30	2471.5	42.7	1147	4	US-10-369-493-11450	Sequence 11450, A
31	2471.5	42.7	1151	4	US-10-369-493-14817	Sequence 14817, A
32	2471.5	42.7	1151	4	US-10-369-493-15006	Sequence 15006, A
33	2470.5	42.7	1152	4	US-10-369-493-12027	Sequence 12027, A
34	2464.5	42.6	1142	4	US-10-282-122A-57942	Sequence 57942, A
35	2464	42.6	1154	4	US-10-724-972A-5609	Sequence 5609, Ap
36	2464	42.6	1175	4	US-10-369-493-6504	Sequence 6504, Ap
37	2463.5	42.6	1142	4	US-10-282-122A-42528	Sequence 42528, A
38	2457	42.5	1178	4	US-10-369-493-21939	Sequence 21939, A
39	2455	42.4	1144	5	US-10-501-282-2136	Sequence 2136, Ap
40	2443	42.2	1167	4	US-10-369-493-22819	Sequence 22819, A
41	2443	42.2	1185	4	US-10-369-493-2488	Sequence 2488, Ap
42	2441	42.2	1181	6	US-11-097-143-1425	Sequence 1425, Ap
43	2441	42.2	1181	6	US-11-097-143-26604	Sequence 26604, A
44	2441	42.2	1181	6	US-11-097-143-26607	Sequence 26607, A
45	2436	42.1	1180	4	US-10-369-493-1491	Sequence 1491, Ap

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OM protein - protein search, using sw model

Run on: February 28, 2006, 10:53:27 ; Search time 19 Seconds  
(without alignments)  
893.235 Million cell updates/sec

Title: US-09-529-043B-2  
Perfect score: 5787  
Sequence: 1 VSTHTSSTLPAFKKILVANR.....RVVVPAAATKVEGGDLIVVVS 1140

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description
	Query	Match	Length	DB	ID	
No.	Score					
1	5784	99.9	1140	6	US-10-858-730-208	Sequence 208, App
2	3799	65.6	1124	6	US-10-858-730-12	Sequence 12, Appl
3	3783.5	65.4	1127	6	US-10-858-730-13	Sequence 13, Appl
4	2464	42.6	1151	6	US-10-793-626-2448	Sequence 2448, Ap
5	975	16.8	472	7	US-11-232-405A-30	Sequence 30, Appl
6	936.5	16.2	453	6	US-10-467-657-1642	Sequence 1642, Ap
7	866	15.0	703	6	US-10-821-234-1317	Sequence 1317, Ap
8	851.5	14.7	453	6	US-10-793-626-804	Sequence 804, App
9	801	13.8	615	7	US-11-232-405A-32	Sequence 32, Appl



10	606.5	10.5	341	6	US-10-793-626-218	Sequence 218, App
11	594	10.3	2256	7	US-11-144-368-4	Sequence 4, Appli
12	594	10.3	2458	7	US-11-186-999-13	Sequence 13, Appl
13	587	10.1	2458	7	US-11-186-999-6	Sequence 6, Appli
14	586.5	10.1	2455	7	US-11-186-999-14	Sequence 14, Appl
15	586.5	10.1	2455	7	US-11-186-999-16	Sequence 16, Appl
16	585.5	10.1	309	6	US-10-793-626-648	Sequence 648, App
17	578.5	10.0	2455	7	US-11-186-999-4	Sequence 4, Appli
18	561.5	9.7	2483	7	US-11-186-999-2	Sequence 2, Appli
19	544	9.4	2458	7	US-11-186-999-11	Sequence 11, Appl
20	534.5	9.2	2348	6	US-10-450-224A-2	Sequence 2, Appli
21	531	9.2	1096	6	US-10-995-561-710	Sequence 710, App
22	528.5	9.1	2456	7	US-11-186-999-8	Sequence 8, Appli
23	528.5	9.1	2456	7	US-11-186-999-10	Sequence 10, Appl
24	498	8.6	472	7	US-11-098-686-10733	Sequence 10733, A
25	255	4.4	1073	7	US-11-253-665-20	Sequence 20, Appl
26	234	4.0	1071	6	US-10-467-657-1654	Sequence 1654, Ap
27	221.5	3.8	1066	7	US-11-055-822-370	Sequence 370, App
28	221.5	3.8	1066	7	US-11-055-822-1002	Sequence 1002, Ap
29	221.5	3.8	1113	7	US-11-055-822-368	Sequence 368, App
30	221.5	3.8	1113	7	US-11-055-822-1000	Sequence 1000, Ap
31	211.5	3.7	6893	7	US-11-205-109-14	Sequence 14, Appl
32	203	3.5	1076	7	US-11-098-686-11184	Sequence 11184, A
33	183.5	3.2	8695	7	US-11-205-109-15	Sequence 15, Appl
34	170.5	2.9	2087	7	US-11-075-185-28	Sequence 28, Appl
35	169.5	2.9	3507	7	US-11-075-185-7	Sequence 7, Appli
36	159.5	2.8	3655	7	US-11-075-185-5	Sequence 5, Appli
37	154.5	2.7	3689	7	US-11-075-185-4	Sequence 4, Appli
38	152	2.6	2004	6	US-10-467-657-84	Sequence 84, Appl
39	152	2.6	2004	6	US-10-467-657-6322	Sequence 6322, Ap
40	151.5	2.6	7102	7	US-11-143-980-48	Sequence 48, Appl
41	147	2.5	7968	7	US-11-143-980-49	Sequence 49, Appl
42	145.5	2.5	3073	7	US-11-143-980-50	Sequence 50, Appl
43	141.5	2.4	1461	7	US-11-052-554A-283	Sequence 283, App
44	139	2.4	1572	7	US-11-143-980-46	Sequence 46, Appl
45	134.5	2.3	1448	6	US-10-485-517-212	Sequence 212, App

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OM protein - protein search, using sw model

Run on: February 28, 2006, 10:47:21 ; Search time 50 Seconds  
(without alignments)  
2193.742 Million cell updates/sec

Title: US-09-529-043B-2  
Perfect score: 5787  
Sequence: 1 VSTHTSSTLPAFKKILVANR.....RVVVPAAATKVEGGDLIVVVS 1140

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query					Description
	No.	Score	Match Length	DB	ID	
1	3712.5	64.2	1127	2	D70671	pyruvate carboxyla
2	2541.5	43.9	1178	1	A47255	pyruvate carboxyla
3	2538.5	43.9	1178	2	JC4391	pyruvate carboxyla
4	2525.5	43.6	1150	2	A83978	pyruvate carboxyla
5	2524	43.6	1148	2	F69685	pyruvate carboxyla
6	2517.5	43.5	1178	1	JC2460	pyruvate carboxyla
7	2493	43.1	1146	2	AH1208	pyruvate carboxyla
8	2491.5	43.1	1144	2	D97227	pyruvate carboxyla
9	2490	43.0	1146	2	AC1565	pyruvate carboxyla
10	2488	43.0	1150	2	G89881	pyruvate carboxyla
11	2473.5	42.7	1174	2	AE2911	pyruvate carboxyla
12	2473.5	42.7	1174	2	C97686	pyruvate carboxyla
13	2464.5	42.6	1158	2	AE3285	pyruvate carboxyla

14	2464	42.6	1175	2	T20346	pyruvate carboxyla
15	2457	42.5	1178	1	QYBYP	pyruvate carboxyla
16	2443	42.2	1185	2	T39734	pyruvate carboxyla
17	2436	42.1	1180	2	S46094	pyruvate carboxyla
18	2417.5	41.8	1195	2	T43735	pyruvate carboxyla
19	2406	41.6	1137	2	E86708	pyruvate carboxyla
20	2115.5	36.6	984	2	T44608	pyruvate carboxyla
21	1079	18.6	501	2	D64453	biotin carboxylase
22	1063.5	18.4	477	2	G70427	biotin carboxylase
23	1036.5	17.9	447	2	AH1923	biotin carboxylase
24	1036.5	17.9	447	2	A53311	biotin carboxylase
25	1035	17.9	472	2	A70432	biotin carboxylase
26	1019	17.6	506	2	D69277	biotin carboxylase
27	997	17.2	491	2	A69123	biotin carboxylase
28	981.5	17.0	448	2	S74380	biotin carboxylase
29	976.5	16.9	471	2	G82966	probable biotin ca
30	975.5	16.9	1095	2	B83471	probable pyruvate
31	971.5	16.8	1078	2	D87647	hypothetical prote
32	961.5	16.6	447	2	B97338	biotin carboxylase
33	959	16.6	667	2	F98286	hypothetical prote
34	959	16.6	677	2	AC2997	hypothetical prote
35	957.5	16.5	444	2	C70444	biotin carboxylase
36	957	16.5	449	2	AI0912	biotin carboxylase
37	951.5	16.4	455	2	B86722	biotin carboxylase
38	949	16.4	449	2	AD0445	biotin carboxylase
39	948.5	16.4	539	2	T07093	acetyl-CoA carboxy
40	946	16.3	444	2	T44813	biotin carboxylase
41	946	16.3	448	1	F64105	biotin carboxylase
42	942.5	16.3	455	2	C95049	acetyl-CoA carboxy
43	942	16.3	450	2	A69581	acetyl-CoA carboxy
44	941.5	16.3	455	2	A97920	biotin carboxylase
45	939.5	16.2	457	2	H71553	probable biotin ca

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 28, 2006, 10:43:56 ; Search time 253 Seconds  
(without alignments)  
3179.060 Million cell updates/sec

Title: US-09-529-043B-2  
Perfect score: 5787  
Sequence: 1 VSTHTSSTLPAFKKILVANR.....RVVVPAAATKVEGGDLIVVVS 1140

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	5784	99.9	1140	2 O54587_CORGL	O54587 corynebacte
2	5755	99.4	1140	2 Q6F5A6_CORGL	Q6f5a6 corynebacte
3	5755	99.4	1140	2 Q8L2G4_CORCT	Q8l2g4 corynebacte
4	5319.5	91.9	1168	2 Q8FRQ0_COREF	Q8frq0 corynebacte
5	5302.5	91.6	1139	2 Q8RQL2_COREF	Q8rql2 corynebacte
6	4647.5	80.3	1141	2 Q6NIX0_CORDI	Q6nix0 corynebacte
7	3847.5	66.5	1133	2 Q5YS01_NOCFA	Q5ys01 nocardia fa
8	3799	65.6	1124	2 Q9RK64_STRCO	Q9rk64 streptomyce
9	3783.5	65.4	1127	2 Q9F843_MYCSM	Q9f843 mycobacteri
10	3768.5	65.1	1127	2 Q744P7_MYCPA	Q744p7 mycobacteri
11	3712.5	64.2	1127	2 Q7TXJ1_MYCBO	Q7txj1 mycobacteri
12	3712.5	64.2	1127	2 P95127_MYCTU	P95127 mycobacteri
13	3646.5	63.0	1131	2 Q4NCP7_MYICC	Q4ncp7 arthrobacte
14	3581	61.9	1134	2 Q6AE43_LEIXX	Q6ae43 leifsonia x
15	3483	60.2	1124	2 Q50450_MYCTU	Q50450 mycobacteri

16	3248	56.1	1131	2	Q83HF3_TROW8	Q83hf3 tropheryma
17	3241	56.0	1131	2	Q83FS5_TROWT	Q83fs5 tropheryma
18	2646	45.7	1148	2	Q67MC6_SYMTH	Q67mc6 symbiobacte
19	2594	44.8	1209	2	Q4NUC5_9DELT	Q4nuc5 anaeromyxob
20	2563	44.3	1148	2	Q74AE8_GEOSL	Q74ae8 geobacter s
21	2560.5	44.2	1193	2	Q4WP18_ASPFU	Q4wp18 aspergillus
22	2556	44.2	1147	2	Q5L116_GEOKA	Q5l116 geobacillus
23	2552	44.1	1178	2	Q8JHF6_CHICK	Q8jhf6 gallus gall
24	2544	44.0	1148	2	Q6HEL7_BACHK	Q6hel7 bacillus th
25	2543	43.9	1148	2	Q635X9_BACCZ	Q635x9 bacillus ce
26	2541.5	43.9	1178	1	PYC_MOUSE	Q05920 mus musculu
27	2540.5	43.9	1178	2	Q7YS28_PIG	Q7ys28 sus scrofa
28	2539	43.9	1148	2	Q4MTD4_BACC	Q4mtd4 bacillus ce
29	2538.5	43.9	1178	2	Q5RKM0_RAT	Q5rkm0 rattus norv
30	2534	43.8	1147	2	Q65K15_BACLD	Q65k15 bacillus li
31	2534	43.8	1148	2	Q732C0_BACC1	Q732c0 bacillus ce
32	2533.5	43.8	1145	2	Q5LU87_SILPO	Q5lu87 silicibacte
33	2528	43.7	1148	2	Q819M9_BACCR	Q819m9 bacillus ce
34	2526	43.6	1148	2	Q81MT6_BACAN	Q81mt6 bacillus an
35	2525.5	43.6	1150	2	Q9K9M0_BACHD	Q9k9m0 bacillus ha
36	2525.5	43.6	1178	2	Q866R1_BOVIN	Q866r1 bos taurus
37	2524.5	43.6	1178	1	PYC_RAT	P52873 rattus norv
38	2524	43.6	1148	1	PYC_BACSU	Q9kwu4 bacillus su
39	2522.5	43.6	1196	2	Q5B4R8_EMENI	Q5b4r8 aspergillus
40	2520.5	43.6	1178	1	PYC_HUMAN	P11498 homo sapien
41	2519.5	43.5	1180	2	Q9DDT1_BRARE	Q9ddt1 brachydanio
42	2511	43.4	1166	2	Q7UES1_RHOBA	Q7ues1 rhodopirell
43	2509.5	43.4	1192	1	PYC_ASPNG	Q9hes8 aspergillus
44	2505	43.3	1147	2	P94448_BACST	P94448 bacillus st
45	2503.5	43.3	1191	2	Q6CAV2_YARLI	Q6cav2 yarrowia li